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AMENDMENTS TO THE CLAIMS

Please incorporate the following amendments to the subject application.

In the Claims:

1. **(Currently Amended)** A method of identifying a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized normalization probe, said method comprising:

(a) identifying a plurality of candidate probe sequences for a target nucleic acid based on at least one selection criterion;

(b) empirically evaluating each of said candidate probe sequences under a plurality of different experimental ~~sets~~ **conditions** to obtain a collection of empirical data values for each of said candidate nucleic acid probe sequences for each of said plurality of different experimental ~~sets~~ **conditions, and for each member of said plurality of different experimental conditions:**

(i) providing an array of candidate nucleic acid probes immobilized on a surface of a solid support, wherein said array includes a substrate surface immobilized nucleic acid candidate probe for each of said identified candidate probe sequences; and

(ii) subjecting said array to said member of said plurality of different experimental conditions;

(c) clustering said candidate probe sequences into one or more groups of candidate probe sequences based on each candidate probe sequence's collection of empirical data values, wherein each of said one or more groups exhibits substantially the same performance across said plurality of experimental ~~sets~~ **conditions**;

(d) evaluating any remaining non-clustering probes for candidate probe sequences that satisfy a signal intensity threshold and exhibit substantially no variation in signal under said plurality of different experimental ~~sets~~ **conditions** to identify any candidate probe sequences of said plurality

that are suitable for use as a substrate surface immobilized normalization probe.

2. (Original) The method according to Claim 1, wherein said at least one selection criterion employed in said identifying step (a) is chosen from:

(i) proximity to the 3' end of said target nucleic acid's corresponding mRNA transcript;

(ii) base composition; and

(iii) lack of homology to other expressed sequences of said target nucleic acid's organism.

3. (Original) The method according to Claim 2, wherein all three of said selection criteria (i), (ii) and (iii) are employed is said identifying step (a).

4. (Original) The method according to Claim 3, wherein said identifying step (a) is further characterized by employing parameters that minimize the number of identified candidate probe sequences that overlap with each other.

5. **(Cancelled)**

6. **(Currently Amended)** The method according to ~~Claim 5~~ **Claim 1**, wherein each member of said plurality of different experimental conditions is a different tissue/cell line differential gene expression assay.

7. (Original) The method according to Claim 1, said clustering step (c) comprises:

(i) obtaining an expression vector for each of said candidate probe sequences using said candidate sequence's collection of empirical data values;

(ii) deriving a similarity matrix for the set of said candidate probe sequences from said candidate probe sequences' expression vectors; and

(iii) grouping said candidate probe sequences based on their derived similarity.

8. (Original) The method according to Claim 7, wherein those candidate probes that have substantially similar expression patterns are grouped together.

9. (Original) The method according to Claim 1, wherein the clustering step employs an affinity threshold or another stringency controlling parameter.

10. **(Currently Amended)** The method according to Claim 1, wherein a candidate probe sequence is considered to exhibit substantially no variation in signal under said plurality of different experimental ~~sets~~ **conditions** if its log ratio is not significantly different than zero ~~across~~ **across** said plurality of different experimental ~~sets~~ **conditions**.

11. (Original) The method according to Claim 10, wherein said log ratio is between about 0.5 and -0.5.

12. **(Currently Amended)** The method according to Claim 1, wherein said ~~purality~~ **plurality** of different experimental ~~sets~~ **conditions** is at least 2.

13. (Original) The method according to Claim 12, wherein if no non-clustering probes are present after said clustering step (c), said evaluating step (d) is not performed.

14. (Original) The method according to Claim 1, wherein at least some of said steps are carried out by a computational analysis system.

15. (Original) A computer-readable medium having recorded thereon a program that identifies a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized normalization probe according to the method of Claim 1.

16. (Original) A computational analysis system comprising a computer-readable medium according to Claim 15.

17. (Withdrawn; **Currently Amended**) A method of producing a nucleic acid array, said method comprising:

~~producing at least two different probe nucleic acids immobilized on a surface of a solid support, wherein at least one of said at least two different probe nucleic acids is a normalization probe that has a sequence of nucleotides identified according to the method of Claim 1~~

(a) identifying a plurality of candidate probe sequences for a target nucleic acid based on at least one selection criterion;

(b) empirically evaluating each of said candidate probe sequences under a plurality of different experimental conditions to obtain a collection of empirical data values for each of said candidate nucleic acid probe sequences for each of said plurality of different experimental conditions;

(c) clustering said candidate probe sequences into one or more groups of candidate probe sequences based on each candidate probe sequence's collection of empirical data values, wherein each of said one or more groups exhibits substantially the same performance across said plurality of experimental conditions; and

(d) evaluating any remaining non-clustering probes for candidate probe sequences that satisfy a signal intensity threshold and exhibit substantially no variation in signal under said plurality of different experimental conditions to identify any candidate probe sequences of said plurality that are suitable for use as a substrate surface immobilized normalization probe,

and producing a nucleic acid array comprising at least two different probe nucleic acids immobilized on a surface of a solid support, wherein at least one of said at least two different probe nucleic acids is a normalization probe that has a sequence of nucleotides identified.

18. (Withdrawn) The method according to Claim 17, wherein said at least two different probe nucleic acids are produced on said surface of said solid support by synthesizing said probe nucleic acids on said surface.

19. (Withdrawn) The method according to Claim 17, wherein said at least two different probe nucleic acids are produced on said surface of said solid support by depositing said at least two different probe nucleic acids onto said surface of said solid support.

20. (Withdrawn) A nucleic acid array produced according to the method of Claim 17.

21 – 25. **(Cancelled)**

26. (New) A method of identifying a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized normalization probe, said method comprising:

(a) identifying a plurality of candidate probe sequences for a target nucleic acid based on at least one selection criterion;

(b) empirically evaluating each of said candidate probe sequences under a plurality of different experimental conditions to obtain a collection of empirical data values for each of said candidate nucleic acid probe sequences for each of said plurality of different experimental conditions;

(c) clustering said candidate probe sequences into one or more groups of candidate probe sequences based on each candidate probe sequence's collection of empirical data values, wherein each of said one or more groups exhibits substantially the same performance across said plurality of experimental conditions;

(d) evaluating any remaining non-clustering probes for candidate probe sequences that satisfy a signal intensity threshold and exhibit substantially no variation in signal under said plurality of different experimental conditions to identify any candidate probe sequences of said plurality that are suitable for use as a substrate surface immobilized normalization probe; and

(e) recording the identified candidate probe sequences on a computer-readable medium.

27. (New) The method according to Claim 26, wherein said at least one selection criterion employed in said identifying step (a) is chosen from:

(i) proximity to the 3' end of said target nucleic acid's corresponding mRNA transcript;

(ii) base composition; and

(iii) lack of homology to other expressed sequences of said target nucleic acid's organism.

28. (New) The method according to Claim 26, said clustering step (c) comprises:

(i) obtaining an expression vector for each of said candidate probe sequences using said candidate sequence's collection of empirical data values;

(ii) deriving a similarity matrix for the set of said candidate probe sequences from said candidate probe sequences' expression vectors; and

(iii) grouping said candidate probe sequences based on their derived similarity.

29. (New) The method according to Claim 28, wherein those candidate probes that have substantially similar expression patterns are grouped together.

30. (New) The method according to Claim 26, wherein at least some of said steps are carried out by a computational analysis system.